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SEQUENCE LISTING

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Ile Thr Thr Ala Val Ala Val Asp Glu	
1705 1710	
cagtcccaac gaaggggtggc cccggatgac ctccgtccgc ccgtgctcgc cgtcggtgaa	6745
cgcgggctgg tcggtgggca ggaagacctc atcgccgaca tcgccctcga cctcgcagct	6805
cgtcagtagg aatgcgcacg ggccgacgag tcgcgctggg caccggggcc agccgcggca	6865
tcggggcggc catcgcagat gcggtggccg cctccggtgc cgccgtaatc gtccactacg	6925
gatccgateg gacggccgcc gctgcggtgt cgacggcatc acggctgccg ggggcctcgc	6985
ggctgcggtc caggccgacc tgtcccgacc cgaggggcct gaagagctga tgcgggagtt	7045
cgactccgcg ctgcacggtc tcgggctcga ccgagggctc gacatcctcg tcaacaacgc	7105
cggaatcagt cggcgcgag cgctcgagcg cgtcactgtc gaggatttcg accgtctggt	7165
cgactcaac cagcgcgccc cgttcttcgt gactcggcat gccctgcccc ggatgcacga	7225
cggcggtcgc atcgtcaaca tttcctccgg atccgccccg tacgccagac ccgacgtcat	7285
cagctacgcc atgaccaagg gggcgatcga ggtgctcacc cgcgccctcg ccgtagacgt	7345
cggcgaacga ggcatacccg ccaacgccgt ggcgccggcc gcgctcgata ccgacatgaa	7405
cgcgactgg cttcgcggtg acgaccatgc ccgcaccacc gccgcgtcca ccactgcact	7465

gcgaaaactc gccaccgcgg aggacatcgc cgcgatcgtg gccttcctcg tcagcgccgc 7525
 cgccggtgcg atcaccgggc aggtcatcga cgccaccaac ggcaaccggc tctaaccaga 7585
 acttaccggg tccc 7599

<210> 2
 <211> 246
 <212> PRT
 <213> Rhodococcus sp.

<400> 2
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 Leu Leu Ala Asn Val Arg Thr Ser Gly Ala Arg Leu Ser Ser Ala Leu
 20 25 30
 Tyr Asp Ile Leu Lys Asn Arg Leu Leu Glu Gly Arg Tyr Ala Ala Gly
 35 40 45
 Glu Lys Ile Val Val Glu Ser Ile Arg Gln Glu Phe Gly Val Ser Lys
 50 55 60
 Gln Pro Val Met Asp Ala Leu Arg Arg Leu Ser Ser Asp Lys Leu Val
 65 70 75 80
 His Ile Val Pro Gln Val Gly Cys Glu Val Val Ser Tyr Ala Pro Arg
 85 90 95
 Glu Val Glu Asp Phe Tyr Thr Leu Phe Gly Gly Phe Glu Gly Thr Ile
 100 105 110
 Ala Ala Val Ala Ala Ser Arg Arg Thr Glu Ala Gln Leu Leu Glu Leu
 115 120 125
 Asp Leu Ile Ser Ala Arg Val Asp Ala Leu Ile Thr Ser His Asp Pro
 130 135 140
 Val Val Arg Ala Arg Gly Tyr Arg Val His Asn Arg Glu Phe His Ala
 145 150 155 160
 Ala Ile His Ala Met Ala His Ser Arg Ile Met Glu Glu Thr Ser Gln
 165 170 175
 Arg Met Trp Asp Leu Ser Asp Phe Leu Ile Asn Thr Thr Gly Ile Thr
 180 185 190
 Asn Pro Leu Ser Ser Ala Leu Pro Asp Arg Gln His Asp His His Glu
 195 200 205
 Ile Thr Glu Ala Ile Arg Asn Arg Asp Ala Ala Ala Ala Arg Glu Ala
 210 215 220
 Met Glu Arg His Ile Val Gly Thr Ile Ala Val Ile Arg Asp Glu Ser
 225 230 235 240

Asn Ala Gln Leu Pro Ser
245

<210> 3

<211> 514

<212> PRT

<213> Rhodococcus sp.

<400> 3

Val Leu Pro Leu Glu Asp Ser Pro Glu Asn Pro Ser Arg Thr Ser Pro
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Glu Glu Arg Ser Gly His Asp Asp Arg Phe Ala Arg Ile Val Leu Arg
20 25 30

Gly Thr Ser Pro Leu Pro Pro Thr Asp Arg Gly Ser Pro Thr Val Ser
35 40 45

Thr Thr Pro Thr Ser Pro Thr Lys Thr Ser Pro Leu Arg Val Ala Met
50 55 60

Ala Ser Phe Ile Gly Thr Thr Val Glu Tyr Tyr Asp Phe Phe Ile Tyr
65 70 75 80

Gly Thr Ala Ala Ala Leu Val Phe Pro Glu Leu Phe Phe Pro Asp Val
85 90 95

Ser Ser Ala Ile Gly Ile Leu Leu Ser Phe Ala Thr Phe Ser Val Gly
100 105 110

Phe Leu Ala Arg Pro Leu Gly Gly Ile Val Phe Gly His Phe Gly Asp
115 120 125

Arg Val Gly Arg Lys Gln Met Leu Val Ile Ser Leu Val Gly Met Gly
130 135 140

Ser Ala Thr Val Leu Met Gly Leu Leu Pro Gly Tyr Ala Gln Ile Gly
145 150 155 160

Ile Ala Ala Pro Ile Leu Leu Thr Leu Leu Arg Leu Val Gln Gly Phe
165 170 175

Ala Val Gly Gly Glu Trp Gly Gly Ala Thr Leu Met Ala Val Glu His
180 185 190

Ala Pro Thr Ala Lys Lys Gly Phe Phe Gly Ser Phe Ser Gln Met Gly
195 200 205

Ala Pro Ala Gly Thr Ser Val Ala Thr Leu Ala Phe Phe Ala Val Ser
210 215 220

Gln Leu Pro Asp Glu Gln Phe Leu Ser Trp Gly Trp Arg Leu Pro Phe
225 230 235 240

Leu Phe Ser Ala Val Leu Ile Val Ile Gly Leu Phe Ile Arg Leu Ser
245 250 255

Leu Ala Glu Ser Pro Asp Phe Ala Glu Val Lys Ala Gln Ser Ala Val
 260 265 270
 Val Arg Met Pro Ile Ala Glu Ala Phe Arg Lys His Trp Lys Glu Ile
 275 280 285
 Leu Leu Ile Ala Gly Thr Tyr Leu Ser Gln Gly Val Phe Ala Tyr Ile
 290 295 300
 Cys Met Ala Tyr Leu Val Ser Tyr Gly Thr Thr Val Ala Gly Ile Ser
 305 310 315 320
 Arg Thr Phe Ala Leu Ala Gly Val Phe Val Ala Gly Ile Val Ala Val
 325 330 335
 Leu Leu Tyr Leu Val Phe Gly Ala Leu Ser Asp Thr Phe Gly Arg Lys
 340 345 350
 Thr Met Tyr Leu Leu Gly Ala Ala Ala Met Gly Val Val Ile Ala Pro
 355 360 365
 Ala Phe Ala Leu Ile Asn Thr Gly Asn Pro Trp Leu Phe Met Ala Ala
 370 375 380
 Gln Val Leu Val Phe Gly Ile Ala Met Ala Pro Ala Ala Gly Val Thr
 385 390 395 400
 Gly Ser Leu Phe Thr Met Val Phe Asp Ala Asp Val Arg Tyr Ser Gly
 405 410 415
 Val Ser Ile Gly Tyr Thr Ile Ser Gln Val Ala Gly Ser Ala Phe Ala
 420 425 430
 Pro Thr Ile Ala Thr Ala Leu Tyr Ala Ser Thr Asn Thr Ser Asn Ser
 435 440 445
 Ile Val Thr Tyr Leu Leu Ile Val Ser Ala Ile Ser Ile Val Ser Val
 450 455 460
 Ile Leu Leu Pro Gly Gly Trp Gly Arg Lys Gly Ala Ala Ser Gln Leu
 465 470 475 480
 Thr Arg Asp Gln Ala Thr Ser Thr Pro Lys Met Pro Asp Thr Glu Thr
 485 490 495
 Phe Ser Thr Arg Thr Val Pro Asp Thr Ala Ala Ser Leu Arg Val Leu
 500 505 510

Asp Lys

<210> 4

<211> 637

<212> PRT

<213> Rhodococcus sp.

<400> 4

Val	Met	Thr	Asp	Met	Ser	Asp	His	Asp	Arg	Thr	Ser	Tyr	Asp	Thr	Asp
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Val	Val	Ile	Val	Gly	Leu	Gly	Pro	Ala	Gly	Gly	Thr	Ala	Ala	Leu	Ala
			20					25					30		
Leu	Ala	Ser	Tyr	Gly	Ile	Arg	Val	His	Ala	Val	Ser	Met	Phe	Pro	Trp
		35					40					45			
Val	Ala	Asn	Ser	Pro	Arg	Ala	His	Ile	Thr	Asn	Gln	Arg	Ala	Val	Glu
	50					55					60				
Val	Leu	Arg	Asp	Leu	Gly	Val	Glu	Asp	Glu	Ala	Arg	Asn	Tyr	Ala	Thr
65				70					75						80
Pro	Trp	Asp	Gln	Met	Gly	Asp	Thr	Leu	Phe	Thr	Thr	Ser	Leu	Ala	Gly
				85					90					95	
Glu	Glu	Ile	Val	Arg	Met	Gln	Thr	Trp	Gly	Thr	Gly	Asp	Ile	Arg	Tyr
			100					105					110		
Gly	Asp	Tyr	Leu	Ser	Gly	Ser	Pro	Cys	Thr	Met	Leu	Asp	Ile	Pro	Gln
		115					120					125			
Pro	Leu	Met	Glu	Pro	Val	Leu	Ile	Lys	Asn	Ala	Ala	Glu	Arg	Gly	Ala
	130					135					140				
Val	Ile	Ser	Phe	Asn	Thr	Glu	Tyr	Leu	Asp	His	Ala	Gln	Asp	Glu	Asp
145					150					155					160
Gly	Val	Thr	Val	Arg	Phe	Arg	Asp	Val	Arg	Ser	Gly	Thr	Val	Phe	Thr
				165					170					175	
Gln	Arg	Ala	Arg	Phe	Leu	Leu	Gly	Phe	Asp	Gly	Ala	Arg	Ser	Lys	Ile
			180					185					190		
Ala	Glu	Gln	Ile	Gly	Leu	Pro	Phe	Glu	Gly	Glu	Leu	Ala	Arg	Ala	Gly
		195					200					205			
Thr	Ala	Tyr	Ile	Leu	Phe	Asn	Ala	Asp	Leu	Ser	Lys	Tyr	Val	Ala	His
	210					215					220				
Arg	Pro	Ser	Ile	Leu	His	Trp	Ile	Val	Asn	Ser	Lys	Ala	Gly	Phe	Gly
225					230					235					240
Glu	Ile	Gly	Met	Gly	Leu	Leu	Arg	Ala	Ile	Arg	Pro	Trp	Asp	Gln	Trp
				245					250					255	
Ile	Ala	Gly	Trp	Gly	Phe	Asp	Met	Ala	Asn	Gly	Glu	Pro	Asp	Val	Ser
			260					265					270		
Asp	Asp	Val	Val	Leu	Glu	Gln	Ile	Arg	Thr	Leu	Val	Gly	Asp	Pro	His
		275					280					285			
Leu	Asp	Val	Glu	Ile	Val	Ser	Arg	Ser	Phe	Trp	Tyr	Val	Asn	Arg	Gln
	290					295					300				

Trp	Ala	Glu	His	Tyr	Gln	Ser	Gly	Arg	Val	Phe	Cys	Gly	Gly	Asp	Ala	
305					310					315					320	
Val	His	Arg	His	Pro	Pro	Ser	Ser	Gly	Leu	Gly	Ser	Asn	Thr	Ser	Met	
				325					330					335		
Gln	Asp	Ala	Phe	Asn	Leu	Ala	Trp	Lys	Ile	Ala	Phe	Val	Val	Lys	Gly	
			340					345					350			
Tyr	Ala	Gly	Pro	Gly	Leu	Leu	Glu	Ser	Tyr	Ser	Pro	Glu	Arg	Val	Pro	
		355					360					365				
Val	Gly	Lys	Gln	Ile	Val	Ala	Arg	Ala	Asn	Gln	Ser	Arg	Lys	Asp	Tyr	
	370					375					380					
Ala	Gly	Leu	Arg	Glu	Trp	Phe	Asp	His	Glu	Ser	Asp	Asp	Pro	Val	Ala	
385					390					395					400	
Ala	Gly	Leu	Ala	Lys	Leu	Lys	Glu	Pro	Ser	Ser	Glu	Gly	Val	Ala	Leu	
				405					410					415		
Arg	Glu	Arg	Leu	Tyr	Glu	Ala	Leu	Glu	Val	Lys	Asn	Ala	Glu	Phe	Asn	
			420					425					430			
Ala	Gln	Gly	Val	Glu	Leu	Asn	Gln	Arg	Tyr	Thr	Ser	Ser	Ala	Val	Val	
		435					440					445				
Pro	Asp	Pro	Glu	Ala	Gly	Glu	Glu	Val	Trp	Val	Arg	Asp	Arg	Glu	Leu	
	450					455					460					
Tyr	Leu	Gln	Ala	Thr	Thr	Arg	Pro	Gly	Ala	Lys	Leu	Pro	His	Ala	Trp	
465					470					475					480	
Leu	Val	Gly	Ala	Asp	Gly	Thr	Arg	Ile	Ser	Thr	Leu	Asp	Val	Thr	Gly	
				485					490					495		
Lys	Gly	Met	Met	Thr	Leu	Leu	Thr	Gly	Leu	Gly	Gly	Gln	Ala	Trp	Lys	
		500						505					510			
Arg	Ala	Ala	Ala	Lys	Leu	Asp	Leu	Pro	Phe	Leu	Arg	Thr	Val	Val	Val	
		515					520					525				
Gly	Glu	Pro	Gly	Thr	Ile	Asp	Pro	Tyr	Gly	Tyr	Trp	Arg	Arg	Val	Arg	
	530					535					540					
Asp	Ile	Asp	Glu	Ala	Gly	Ala	Leu	Leu	Val	Arg	Pro	Asp	Gly	Tyr	Val	
545					550					555					560	
Ala	Trp	Arg	His	Ser	Ala	Pro	Val	Trp	Asp	Asp	Thr	Glu	Ala	Leu	Thr	
				565					570					575		
Ser	Leu	Glu	Asn	Ala	Leu	Thr	Ala	Val	Leu	Asp	His	Ser	Ala	Ser	Asp	
			580					585					590			
Asn	Gly	Asn	Pro	Ser	Gly	Thr	Asn	Glu	Pro	Gln	Tyr	Ser	Thr	Arg	Ala	
		595					600						605			

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Ser Ala Thr Arg Thr Thr Thr Val Glu Gly Glu Asn Arg
625 630 635

<210> 5

<211> 314

<212> PRT

<213> Rhodococcus sp.

<400> 5

Met Pro Val Ala Leu Cys Ala Met Ser His Ser Pro Leu Met Gly Arg
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Asn Asp Pro Glu Gln Glu Val Ile Asp Ala Val Asp Ala Ala Phe Asp
20 25 30

His Ala Arg Arg Phe Val Ala Asp Phe Ala Pro Asp Leu Ile Val Ile
35 40 45

Phe Ala Pro Asp His Tyr Asn Gly Val Phe Tyr Asp Leu Leu Pro Pro
50 55 60

Phe Cys Ile Gly Ala Ala Ala Gln Ser Val Gly Asp Tyr Gly Thr Glu
65 70 75 80

Ala Gly Pro Leu Asp Val Asp Arg Asp Ala Ala Tyr Ala Val Ala Arg
85 90 95

Asp Val Leu Asp Ser Gly Ile Asp Val Ala Phe Ser Glu Arg Met His
100 105 110

Val Asp His Gly Phe Ala Gln Ala Leu Gln Leu Leu Val Gly Ser Ile
115 120 125

Thr Ala Val Pro Thr Val Pro Ile Phe Ile Asn Ser Val Ala Glu Pro
130 135 140

Leu Gly Pro Val Ser Arg Val Arg Leu Leu Gly Glu Ala Val Gly Arg
145 150 155 160

Ala Ala Ala Lys Leu Asp Lys Arg Val Leu Phe Val Gly Ser Gly Gly
165 170 175

Leu Ser His Asp Pro Pro Val Pro Gln Phe Ala Thr Ala Pro Glu Glu
180 185 190

Val Arg Glu Arg Leu Ile Asp Gly Arg Asn Pro Ser Ala Ala Glu Arg
195 200 205

Asp Ala Arg Glu Gln Arg Val Ile Thr Ala Gly Arg Asp Phe Ala Ala
210 215 220

Gly Thr Ala Ala Ile Gln Pro Leu Asn Pro Glu Trp Asp Arg His Leu
225 230 235 240

Leu	Asp	Val	Leu	Ala 245	Ser	Gly	Asp	Leu	Glu	Gln	Ile	Asp	Ala	Trp	Thr
Asn	Asp	Trp	Phe	Val	Glu	Gln	Ala	Gly 265	His	Ser	Ser	His	Glu	Val	Arg
Thr	Trp	Ile	Ala	Ala	Tyr	Ala	Ala 280	Met	Ser	Ala	Ala	Gly	Lys	Tyr	Arg
Val	Thr	Ser	Thr	Phe	Tyr	Arg	Glu	Ile	His	Glu	Trp	Ile	Ala	Gly	Phe
Gly	Ile	Thr	Thr	Ala	Val	Ala	Val	Asp	Glu						

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<210> 6
<211> 870
<212> DNA
<213> Rhodococcus sp.
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<220>
<221> CDS
<222> (1) .. (867)
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Met	Thr	Arg	Pro	Tyr	Thr	Ser	Val	Trp	Asp	Asp	Leu	Asn	Gln	Val	Glu	
1				5				10				15				
ttc	agc	cag	gga	ttc	atc	cag	gcc	ggc	ccc	tac	cgg	acc	cga	tac	ctg	96
Phe	Ser	Gln	Gly	Phe	Ile	Gln	Ala	Gly	Pro	Tyr	Arg	Thr	Arg	Tyr	Leu	
20				25				30								
cac	gcc	ggc	gat	tcg	tcc	aag	ccc	acg	ctg	atc	ctg	ctg	cac	ggc	atc	144
His	Ala	Gly	Asp	Ser	Ser	Lys	Pro	Thr	Leu	Ile	Leu	Leu	His	Gly	Ile	
35				40				45								
acc	ggc	cac	gcc	gag	gcg	tac	gtg	cgc	aat	ctg	cgc	tcg	cat	tcc	gag	192
Thr	Gly	His	Ala	Glu	Ala	Tyr	Val	Arg	Asn	Leu	Arg	Ser	His	Ser	Glu	
50				55				60								
cac	ttc	aac	gtc	tgg	gca	atc	gac	ttc	atc	ggc	cac	ggc	tat	tcg	acc	240
His	Phe	Asn	Val	Trp	Ala	Ile	Asp	Phe	Ile	Gly	His	Gly	Tyr	Ser	Thr	
65				70				75				80				
aag	ccc	gac	cac	ccg	ctc	gag	atc	aag	cac	tac	atc	gac	cag	gtg	ctg	288
Lys	Pro	Asp	His	Pro	Leu	Glu	Ile	Lys	His	Tyr	Ile	Asp	Gln	Val	Leu	
85				90				95								
cag	ttg	ctg	gac	gcc	atc	ggc	gtc	gag	aag	gcc	tcg	ttt	tcc	ggg	gag	336
Gln	Leu	Leu	Asp	Ala	Ile	Gly	Val	Glu	Lys	Ala	Ser	Phe	Ser	Gly	Glu	
100				105				110								

tct ctc ggc ggt tgg gtc acc gcc cag ttc gcg cac gac cat ccc gag	384
Ser Leu Gly Gly Trp Val Thr Ala Gln Phe Ala His Asp His Pro Glu	
115 120 125	
aag gtc gac cgg atc gtg ctc aac acc atg ggc ggc acc atg gcc aac	432
Lys Val Asp Arg Ile Val Leu Asn Thr Met Gly Gly Thr Met Ala Asn	
130 135 140	
cct cag gtg atg gaa cgt ctc tat acc ctg tcg atg gaa gcg gcg aag	480
Pro Gln Val Met Glu Arg Leu Tyr Thr Leu Ser Met Glu Ala Ala Lys	
145 150 155 160	
gac ccg agc tgg gaa cgc gtc aaa gca cgc ctc gaa tgg ctc atg gcc	528
Asp Pro Ser Trp Glu Arg Val Lys Ala Arg Leu Glu Trp Leu Met Ala	
165 170 175	
gac ccg acc atg gtc acc gac gac ctg atc cgc acc cgc cag gcc atc	576
Asp Pro Thr Met Val Thr Asp Asp Leu Ile Arg Thr Arg Gln Ala Ile	
180 185 190	
ttc cag cag ccg gat tgg ctc aag gcc tgc gag atg aac atg gca ctg	624
Phe Gln Gln Pro Asp Trp Leu Lys Ala Cys Glu Met Asn Met Ala Leu	
195 200 205	
cag gac ctc gaa acc cgc aag cgg aac atg atc acc gac gcc act ctc	672
Gln Asp Leu Glu Thr Arg Lys Arg Asn Met Ile Thr Asp Ala Thr Leu	
210 215 220	
aac ggc atc acg gtg ccc gcg atg gtg ctg tgg acc acc aag gac ccc	720
Asn Gly Ile Thr Val Pro Ala Met Val Leu Trp Thr Thr Lys Asp Pro	
225 230 235 240	
tcc ggt ccg gtc gac gaa gcc aag cgc atc gcc tcc cac atc ccg ggc	768
Ser Gly Pro Val Asp Glu Ala Lys Arg Ile Ala Ser His Ile Pro Gly	
245 250 255	
gcc aag ctg gcc atc atg gag aac tgt ggc cac tgg ccc cag tac gag	816
Ala Lys Leu Ala Ile Met Glu Asn Cys Gly His Trp Pro Gln Tyr Glu	
260 265 270	
gac ccc gag acc ttc aac aag ctg cat ctg gac ttc ctc ctc ggt cgc	864
Asp Pro Glu Thr Phe Asn Lys Leu His Leu Asp Phe Leu Leu Gly Arg	
275 280 285	
agc tga	870
Ser	

<210> 7

<211> 289

<212> PRT

<213> Rhodococcus sp.

<400> 7

Met Thr Arg Pro Tyr Thr Ser Val Trp Asp Asp Leu Asn Gln Val Glu
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Phe Ser Gln Gly Phe Ile Gln Ala Gly Pro Tyr Arg Thr Arg Tyr Leu
 20 25 30
 His Ala Gly Asp Ser Ser Lys Pro Thr Leu Ile Leu Leu His Gly Ile
 35 40 45
 Thr Gly His Ala Glu Ala Tyr Val Arg Asn Leu Arg Ser His Ser Glu
 50 55 60
 His Phe Asn Val Trp Ala Ile Asp Phe Ile Gly His Gly Tyr Ser Thr
 65 70 75 80
 Lys Pro Asp His Pro Leu Glu Ile Lys His Tyr Ile Asp Gln Val Leu
 85 90 95
 Gln Leu Leu Asp Ala Ile Gly Val Glu Lys Ala Ser Phe Ser Gly Glu
 100 105 110
 Ser Leu Gly Gly Trp Val Thr Ala Gln Phe Ala His Asp His Pro Glu
 115 120 125
 Lys Val Asp Arg Ile Val Leu Asn Thr Met Gly Gly Thr Met Ala Asn
 130 135 140
 Pro Gln Val Met Glu Arg Leu Tyr Thr Leu Ser Met Glu Ala Ala Lys
 145 150 155 160
 Asp Pro Ser Trp Glu Arg Val Lys Ala Arg Leu Glu Trp Leu Met Ala
 165 170 175
 Asp Pro Thr Met Val Thr Asp Asp Leu Ile Arg Thr Arg Gln Ala Ile
 180 185 190
 Phe Gln Gln Pro Asp Trp Leu Lys Ala Cys Glu Met Asn Met Ala Leu
 195 200 205
 Gln Asp Leu Glu Thr Arg Lys Arg Asn Met Ile Thr Asp Ala Thr Leu
 210 215 220
 Asn Gly Ile Thr Val Pro Ala Met Val Leu Trp Thr Thr Lys Asp Pro
 225 230 235 240
 Ser Gly Pro Val Asp Glu Ala Lys Arg Ile Ala Ser His Ile Pro Gly
 245 250 255
 Ala Lys Leu Ala Ile Met Glu Asn Cys Gly His Trp Pro Gln Tyr Glu
 260 265 270
 Asp Pro Glu Thr Phe Asn Lys Leu His Leu Asp Phe Leu Leu Gly Arg
 275 280 285

Ser

<210> 8
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic olig OHP3

<400> 8
atcgaattcg gatccatgac caccacc 27

<210> 9
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic olig OHP4

<400> 9
atcgcggccg ctctagacta actgcagggc gccaaagctcg gcag 44

<210> 10
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic olig C11

<400> 10
atcgaattcg gatccacgag agag 24

<210> 11
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic olig C12

<400> 11
atccggccgc gctctagagt acgcaagct 29

<210> 12
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic olig op1

<400> 12
 atcctcgaga ccccgataacc 20

<210> 13
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic olig op2

<400> 13
 atcgtcgacc gctaccc 17

<210> 14
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic olig CaMVop2

<400> 14
 tccactgacg taagggatga cgcacaatcc cactatcctt cgcaagaccc 50

<210> 15
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic olig CaMVop3

<400> 15
 atgctagacg tctagttcag acgctactta tatagaggaa gggctcttgcg 50

<210> 16
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic olig CaMVop4

<400> 16
 cgtctagcat tctagttgag gaagttcatt tcatttggag aggac 45

<210> 17
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic olig CaMVopF1

<400> 17

atcgatatct ccactgacgt aag

23

<210> 18

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic olig CaMVopR1

<400> 18

gatggatccg tcctctccaa atga

24

<210> 19

<211> 470

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Promoter

<400> 19

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acctcctcgg	attccattgc	ccagctatct	gtcacttcat	cgaaaggaca	gtagaaaagg	180
aagatggctt	ctacaaatgc	catcattgcg	ataaaggaaa	ggctatcggt	caagaatgcc	240
tctaccgaca	gtggtcctca	agatgtaccc	ccaccacaga	ggaacatcgt	ggaaaaagaa	300
gacgttccaa	ccacgtcttc	aaagcaagtg	gattgatgtg	atatctccac	tgacgtaagg	360
gatgacgcac	aatcccacta	tccttcgcaa	gacccttcct	ctatataagt	agcgtctgaa	420
ctagacgtct	agcattctag	ttgaggaagt	tcatttcatt	tgagaggagc		470